

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,286
Source: IFWp
Date Processed by STIC: 5/24/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 05/24/2006

PATENT APPLICATION: US/10/579,286

TIME: 12:21:38

Input Set : A:\39618a.txt

Output Set: N:\CRF4\05242006\J579286.raw

3 <110> APPLICANT: ANDREEV, et al.

5 <120> TITLE OF INVENTION: METHODS FOR IDENTIFYING MODULATORS OF ACTIVE KIT
TYROSINE KINASE

6 RECEPTOR

8 <130> FILE REFERENCE: 30694/39618A

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/579,286

C--> 10 <141> CURRENT FILING DATE: 2006-05-15

10 <150> PRIOR APPLICATION NUMBER: US 60/526,930

11 <151> PRIOR FILING DATE: 2003-12-04

13 <160> NUMBER OF SEQ ID NOS: 6

15 <170> SOFTWARE: PatentIn version 3.2

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 5084

19 <212> TYPE: DNA

20 <213> ORGANISM: Homo sapiens

22 <220> FEATURE:

23 <221> NAME/KEY: CDS

24 <222> LOCATION: (22)..(2952)

26 <400> SEQUENCE: 1

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31 ctc tgc gtt ctg ctc cta ctg ctt cgc gtc cag aca ggc tct tct caa      99
32 Leu Cys Val Leu Leu Leu Leu Arg Val Gln Thr Gly Ser Ser Gln
33                               15                               20                               25
35 cca tct gtg agt cca ggg gaa ccg tct cca tcc atc cat cca gga      147
36 Pro Ser Val Ser Pro Gly Glu Pro Ser Pro Pro Ser Ile His Pro Gly
37                               30                               35                               40
39 aaa tca gac tta ata gtc cgc gtg ggc gac gag att agg ctg tta tgc      195
40 Lys Ser Asp Leu Ile Val Arg Val Gly Asp Glu Ile Arg Leu Leu Cys
41                               45                               50                               55
43 act gat ccg ggc ttt gtc aaa tgg act ttt gag atc ctg gat gaa acg      243
44 Thr Asp Pro Gly Phe Val Lys Trp Thr Phe Glu Ile Leu Asp Glu Thr
45                               60                               65                               70
47 aat gag aat aag cag aat gaa tgg atc acg gaa aag gca gaa gcc acc      291
48 Asn Glu Asn Lys Gln Asn Glu Trp Ile Thr Glu Lys Ala Glu Ala Thr
49 75                               80                               85                               90
51 aac acc ggc aaa tac acg tgc acc aac aaa cac ggc tta agc aat tcc      339
52 Asn Thr Gly Lys Tyr Thr Cys Thr Asn Lys His Gly Leu Ser Asn Ser
53                               95                               100                               105
55 att tat gtg ttt gtt aga gat cct gcc aag ctt ttc ctt gtt gac cgc      387
56 Ile Tyr Val Phe Val Arg Asp Pro Ala Lys Leu Phe Leu Val Asp Arg
57                               110                               115                               120
59 tcc ttg tat ggg aaa gaa gac aac gac acg ctg gtc cgc tgt cct ctc      435

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64	Thr	Asp	Pro	Glu	Val	Thr	Asn	Tyr	Ser	Leu	Lys	Gly	Cys	Gln	Gly	Lys	
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73					175					180					185		
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77				190						195					200		
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80	Lys	Val	Arg	Pro	Ala	Phe	Lys	Ala	Val	Pro	Val	Val	Ser	Val	Ser	Lys	
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83	gca	agc	tat	ctt	ctt	agg	gaa	ggg	gaa	gaa	ttc	aca	gtg	acg	tgc	aca	723
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93				255						260					265		
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104	Ala	Asn	Val	Thr	Thr	Thr	Leu	Glu	Val	Val	Asp	Lys	Gly	Phe	Ile	Asn	
105			300				305					310					
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108	Ile	Phe	Pro	Met	Ile	Asn	Thr	Thr	Val	Phe	Val	Asn	Asp	Gly	Glu	Asn	
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112	Val	Asp	Leu	Ile	Val	Glu	Tyr	Glu	Ala	Phe	Pro	Lys	Pro	Glu	His	Gln	
113				335						340					345		
115	cag	tgg	atc	tat	atg	aac	aga	acc	ttc	act	gat	aaa	tgg	gaa	gat	tat	1107
116	Gln	Trp	Ile	Tyr	Met	Asn	Arg	Thr	Phe	Thr	Asp	Lys	Trp	Glu	Asp	Tyr	
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119	ccc	aag	tct	gag	aat	gaa	agt	aat	atc	aga	tac	gta	agt	gaa	ctt	cat	1155
120	Pro	Lys	Ser	Glu	Asn	Glu	Ser	Asn	Ile	Arg	Tyr	Val	Ser	Glu	Leu	His	
121			365					370						375			
123	cta	acg	aga	tta	aaa	ggc	acc	gaa	gga	ggc	act	tac	aca	ttc	cta	gtg	1203
124	Leu	Thr	Arg	Leu	Lys	Gly	Thr	Glu	Gly	Gly	Thr	Tyr	Thr	Phe	Leu	Val	

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131	aca aaa cca gaa atc ctg act tac gac agg ctc gtg aat ggc atg ctc	1299		
132	Thr Lys Pro Glu Ile Leu Thr Tyr Asp Arg Leu Val Asn Gly Met Leu			
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135	caa tgt gtg gca gca gga ttc cca gag ccc aca ata gat tgg tat ttt	1347		
136	Gln Cys Val Ala Ala Gly Phe Pro Glu Pro Thr Ile Asp Trp Tyr Phe			
137		430	435	440
139	tgt cca gga act gag cag aga tgc tct gct tct gta ctg cca gtg gat	1395		
140	Cys Pro Gly Thr Glu Gln Arg Cys Ser Ala Ser Val Leu Pro Val Asp			
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143	gtg cag aca cta aac tca tct ggg cca ccg ttt gga aag cta gtg gtt	1443		
144	Val Gln Thr Leu Asn Ser Ser Gly Pro Pro Phe Gly Lys Leu Val Val			
145		460	465	470
147	cag agt tct ata gat tct agt gca ttc aag cac aat ggc acg gtt gaa	1491		
148	Gln Ser Ser Ile Asp Ser Ser Ala Phe Lys His Asn Gly Thr Val Glu			
149	475	480	485	490
151	tgt aag gct tac aac gat gtg ggc aag act tct gcc tat ttt aac ttt	1539		
152	Cys Lys Ala Tyr Asn Asp Val Gly Lys Thr Ser Ala Tyr Phe Asn Phe			
153		495	500	505
155	gca ttt aaa ggt aac aac aaa gag caa atc cat ccc cac acc ctg ttc	1587		
156	Ala Phe Lys Gly Asn Asn Lys Glu Gln Ile His Pro His Thr Leu Phe			
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159	act cct ttg ctg att ggt ttc gta atc gta gct ggc atg atg tgc att	1635		
160	Thr Pro Leu Leu Ile Gly Phe Val Ile Val Ala Gly Met Met Cys Ile			
161		525	530	535
163	att gtg atg att ctg acc tac aaa tat tta cag aaa ccc atg tat gaa	1683		
164	Ile Val Met Ile Leu Thr Tyr Lys Tyr Leu Gln Lys Pro Met Tyr Glu			
165		540	545	550
167	gta cag tgg aag gtt gtt gag gag ata aat gga aac aat tat gtt tac	1731		
168	Val Gln Trp Lys Val Val Glu Glu Ile Asn Gly Asn Asn Tyr Val Tyr			
169	555	560	565	570
171	ata gac cca aca caa ctt cct tat gat cac aaa tgg gag ttt ccc aga	1779		
172	Ile Asp Pro Thr Gln Leu Pro Tyr Asp His Lys Trp Glu Phe Pro Arg			
173		575	580	585
175	aac agg ctg agt ttt ggg aaa acc ctg ggt gct gga gct ttc ggg aag	1827		
176	Asn Arg Leu Ser Phe Gly Lys Thr Leu Gly Ala Gly Ala Phe Gly Lys			
177		590	595	600
179	gtt gtt gag gca act gct tat ggc tta att aag tca gat gcg gcc atg	1875		
180	Val Val Glu Ala Thr Ala Tyr Gly Leu Ile Lys Ser Asp Ala Ala Met			
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183	act gtc gct gta aag atg ctc aag ccg agt gcc cat ttg aca gaa cgg	1923		
184	Thr Val Ala Val Lys Met Leu Lys Pro Ser Ala His Leu Thr Glu Arg			
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187	gaa gcc ctc atg tct gaa ctc aaa gtc ctg agt tac ctt ggt aat cac	1971		
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195	ctg	gtc	att	aca	gaa	tat	tgt	tgc	tat	ggg	gat	ctt	ttg	aat	ttt	ttg	2067
196	Leu	Val	Ile	Thr	Glu	Tyr	Cys	Cys	Tyr	Gly	Asp	Leu	Leu	Asn	Phe	Leu	
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199	aga	aga	aaa	cgt	gat	tca	ttt	att	tgt	tca	aag	cag	gaa	gat	cat	gca	2115
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203	gaa	gct	gca	ctt	tat	aag	aat	ctt	ctg	cat	tca	aag	gag	tct	tcc	tgc	2163
204	Glu	Ala	Ala	Leu	Tyr	Lys	Asn	Leu	Leu	His	Ser	Lys	Glu	Ser	Ser	Cys	
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211	gtt	gtc	cca	acc	aag	gcc	gac	aaa	agg	aga	tct	gtg	aga	ata	ggc	tca	2259
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220	Ala	Leu	Asp	Leu	Glu	Asp	Leu	Leu	Ser	Phe	Ser	Tyr	Gln	Val	Ala	Lys	
221		765					770					775					
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224	Gly	Met	Ala	Phe	Leu	Ala	Ser	Lys	Asn	Cys	Ile	His	Arg	Asp	Leu	Ala	
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227	gcc	aga	aat	atc	ctc	ctt	act	cat	ggg	cgg	atc	aca	aag	att	tgt	gat	2451
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235	gga	aac	gct	cga	cta	cct	gtg	aag	tgg	atg	gca	cct	gaa	agc	att	ttc	2547
236	Gly	Asn	Ala	Arg	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	
237			830					835				840					
239	aac	tgt	gta	tac	acg	ttt	gaa	agt	gac	gtc	tgg	tcc	tat	ggg	att	ttt	2595
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243	ctt	tgg	gag	ctg	ttc	tct	tta	gga	agc	agc	ccc	tat	cct	gga	atg	ccg	2643
244	Leu	Trp	Glu	Leu	Phe	Ser	Leu	Gly	Ser	Ser	Pro	Tyr	Pro	Gly	Met	Pro	
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247	gtc	gat	tct	aag	ttc	tac	aag	atg	atc	aag	gaa	ggc	ttc	cgg	atg	ctc	2691
248	Val	Asp	Ser	Lys	Phe	Tyr	Lys	Met	Ile	Lys	Glu	Gly	Phe	Arg	Met	Leu	
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251	agc	cct	gaa	cac	gca	cct	gct	gaa	atg	tat	gac	ata	atg	aag	act	tgc	2739
252	Ser	Pro	Glu	His	Ala	Pro	Ala	Glu	Met	Tyr	Asp	Ile	Met	Lys	Thr	Cys	
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260	Leu	Ile	Glu	Lys	Gln	Ile	Ser	Glu	Ser	Thr	Asn	His	Ile	Tyr	Ser	Asn	
261			925				930				935						
263	tta	gca	aac	tgc	agc	ccc	aac	cga	cag	aag	ccc	gtg	gta	gac	cat	tct	2883
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265		940				945				950							
267	gtg	cgg	atc	aat	tct	gtc	ggc	agc	acc	gct	tcc	tcc	tcc	cag	cct	ctg	2931
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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date